

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: NAGATA, Shigekazu
ITO, Naoto
YONEHARA, Shin
- (ii) TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
ANTIGEN
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
 - (B) STREET: P.O. BOX 747
 - (C) CITY: FALLS CHURCH
 - (D) STATE: VA
 - (E) COUNTRY: USA
 - (F) ZIP: 22040-0747
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/468,560
 - (B) FILING DATE: 06-JUN-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: MURPHY JR., GERLAD M.
 - (B) REGISTRATION NUMBER: 28,977
 - (C) REFERENCE/DOCKET NUMBER: 20-4393P
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 703-205-8000
 - (B) TELEFAX: 703-205-8050

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 195..1202
- (ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 195..242

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 243..1199

(ix) FEATURE:

(A) NAME/KEY: polyA_site
(B) LOCATION: 1831..1836

(ix) FEATURE:

(A) NAME/KEY: polyA_site
(B) LOCATION: 2352..2357

(ix) FEATURE:

(A) NAME/KEY: polyA_site
(B) LOCATION: 2518..2532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACGCTTCTG GGGAGTGAGG GAAGCGGTTT ACGAGTGA CTGCTGGAGC CTCAGGGGCG	60
GGCACTGGCA CGGAACACAC CCTGAGGCCA GCCCTGGCTG CCCAGGCGGA GCTGCCTCTT	120
CTCCCGCGGG TTGGTGGACC CGCTCAGTAC GGAGTTGGGG AAGCTCTTTC ACTTCGGAGG	180
ATTGCTCAAC AACC ATG CTG GGC ATC TGG ACC CTC CTA CCT CTG GTT CTT	230
Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu	-5
-16 -15 -10	
ACG TCT GTT GCT AGA TTA TCG TCC AAA AGT GTT AAT GCC CAA GTG ACT	278
Thr Ser Val Ala Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr	10
1 5	
GAC ATC AAC TCC AAG GGA TTG GAA TTG AGG AAG ACT GTT ACT ACA GTT	326
Asp Ile Asn Ser Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val	25
15 20	
GAG ACT CAG AAC TTG GAA GGC CTG CAT CAT GAT GGC CAA TTC TGC CAT	374
Glu Thr Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His	40
30 35	
AAG CCC TGT CCT CCA GGT GAA AGG AAA GCT AGG GAC TGC ACA GTC AAT	422
Lys Pro Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn	60
45 50 55	
GGG GAT GAA CCA GAC TGC GTG CCC TGC CAA GAA GGG AAG GAG TAC ACA	470
Gly Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr	75
65 70	
GAC AAA GCC CAT TTT TCT TCC AAA TGC AGA AGA TGT AGA TTG TGT GAT	518
Asp Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp	90
80 85	
GAA GGA CAT GGC TTA GAA GTG GAA ATA AAC TGC ACC CGG ACC CAG AAT	566
Glu Gly His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn	105
95 100	
ACC AAG TGC AGA TGT AAA CCA AAC TTT TTT TGT AAC TCT ACT GTA TGT	614

00004987 062101

Thr Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys	110	115	120	
GAA CAC TGT GAC CCT TGC ACC AAA TGT GAA CAT GGA ATC ATC AAG GAA	125	130	135	140
Glu His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu				
TGC ACA CTC ACC AGC AAC ACC AAG TGC AAA GAG GAA GGA TCC AGA TCT		145	150	155
Cys Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser				
AAC TTG GGG TGG CTT TGT CTT CTT CTT TTG CCA ATT CCA CTA ATT GTT		160	165	170
Asn Leu Gly Trp Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val				
TGG CTG AAG AGA AAG GAA GTA CAG AAA ACA TGC AGA AAG CAC AGA AAG		175	180	185
Trp Val Lys Arg Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys				
GAA AAC CAA GGT TCT CAT GAA TCT CCA ACC TTA AAT CCT GAA ACA GTG		190	195	200
Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val				
GCA ATA AAT TTA TCT GAT GTT GAC TTG AGT AAA TAT ATC ACC ACT ATT		205	210	215
Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile				
GCT GGA GTC ATG ACA CTA AGT CAA GTT AAA GGC TTT GTT CGA AAG AAT		225	230	235
Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn				
GGT GTC AAT GAA GCC AAA ATA GAT GAG ATC AAG AAT GAC AAT GTC CAA		240	245	250
Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln				
GAC ACA GCA GAA CAG AAA GTT CAA CTG CTT CGT AAT TGG CAT CAA CTT		255	260	265
Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu				
CAT GGA AAG AAA GAA GCG TAT GAC ACA TTG ATT AAA GAT CTC AAA AAA		270	275	280
His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys				
GCC AAT CTT TGT ACT CTT GCA GAG AAA ATT CAG ACT ATC ATC CTC AAG		285	290	295
Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys				
GAC ATT ACT AGT GAC TCA GAA AAT TCA AAC TTC AGA AAT GAA ATC CAA		305	310	315
Asp Ile Thr Ser Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln				
AGC TTG GTC TAG AGTGAAAAAC AACAAATTCA GTTCTGAGTA TATGCAATTA				
Ser Leu Val				
GTGTTTGAAA AGATTCTTAA TAGCTGGCTG TAAATACTGC TTGGTTTTTT ACTGGGTACA				
TTTTATCATT TATTAGCGCT GAAGAGCCAA CATATTTGTA GATTTTTAAT ATCTCATGAT				
TCTGCCTCCA AGGATGTTTA AAATCTAGTT GGGAAAACAA ACTTCATCAA GAGTAAATGC				

AGTGGCATGC TAAGTACCCA AATAGGAGTG TATGCAGAGG ATGAAAGATT AAGATTATGC 1482
TCTGGCATCT AACATATGAT TCTGTAGTAT GAATGTAATC AGTGTATGTT AGTACAAATG 1542
TCTATCCACA GGCTAACCCC ACTCTATGAA TCAATAGAAG AAGCTATGAC CTTTGTCTGA 1602
AATATCAGTT ACTGAAACAGG CAGGCCACTT TGGCTCTAAA TTACCTCTGA TAATTTCTAGA 1662
GATTTTACCA TATTTCTAAA CTTTGTCTTAT AACTCTGAGA AGATCATATT TATGTAAAGT 1722
ATATGTATTT GAGTGCAGAA TTAAATAAG GCTCTACCTC AAAGACCTTT GCACAGTTA 1782
TTGGTGTCTAT ATTATACAAT ATTTCAATTG TGAATTCACA TAGAAAACAT TAAATTATAA 1842
TGTTTGACTA TTATATATGT GTATGCATTT TACTGGCTCA AAACCTACCTA CTTCTTTCTC 1902
AGGCATCAAA AGCATTTTGA GCAGGAGAGT ATTACTAGAG CTTTGCCACC TCTCCATTTT 1962
TGCCTTGGTG CTCATCTTAA TGGCCTAATG CACCCCCAAA CATGGAAATA TCACCAAAAA 2022
ATACTTAATA GTCCACCAAA AGGCAAGACT GCCCTTAGAA ATTCTAGCCT GGTTTGGAGA 2082
TACTAACTGC TCTCAGAGAA AGTAGCTTTG TGACATGTCA TGAACCCATG TTTGCAATCA 2142
AAGATGATAA AATAGATTCT TATTTTCCC CCACCCCCGA AAATGTTCAA TAATGTCCCA 2202
TGTAACCT GCTACAAATG GCAGCTTATA CATAGCAATG GTAAATCAT CATCTGGATT 2262
TAGGAATTGC TCTTGTCTATA CCCTCAAGTT TCTAAGATTT AAGATTCTCC TTACTACTAT 2322
CCTACGTTTA AATATCTTTG AAAGTTTGTA TTAAATGTGA ATTTTAAGAA ATAATATTTA 2382
TATTTCTGTA AATGTAACT GTGAAGATAG TTATAAACTG AAGCAGATAC CTGGAACCAC 2442
CTAAAGAACT TCCATTTATG GAGGATTTTT TTGCCCCCTG TGTTTGGAAT TATAAAATAT 2502
AGGTAAAGT ACGTAATTAA ATAATGTTTT TG 2534

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
-16 -15 -10 -5
Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
1 5 10 15
Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
20 25 30
Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
35 40 45

09884987-062101

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
50 55 60

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
65 70 75 80

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
85 90 95

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
100 105 110

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
115 120 125

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
130 135 140

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
145 150 155 160

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
165 170 175

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
180 185 190

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu
195 200 205

Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met
210 215 220

Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu
225 230 235 240

Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu
245 250 255

Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys
260 265 270

Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys
275 280 285

Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser
290 295 300

Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
305 310 315

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro
1 5 10 15
Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp
20 25 30
Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys
35 40 45
Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly
50 55 60
His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys
65 70 75 80
Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His
85 90 95
Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr
100 105 110
Leu Thr Ser Asn Thr Lys Cys
115

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys
1 5 10 15
Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly
20 25 30
Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
35 40 45
Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg
50 55 60
Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp
65 70 75 80

Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu
85 90 95
Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val
100 105 110
His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala
115 120 125
Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys
130 135 140
Lys Ser Leu Glu Cys Thr Lys Leu Cys
145 150

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
1 5 10 15
Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
20 25 30
Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
35 40 45
Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Asp
50 55 60
Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
65 70 75 80
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
85 90 95
Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
100 105 110
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
115 120 125
Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
130 135 140
Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
145 150 155 160
Val Cys Thr

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala
1 5 10 15
Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr
20 25 30
Val Cys Glu Pro Cys Leu Asp Ser Val Thr Ser Ser Asp Val Val Ser
35 40 45
Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser
50 55 60
Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala
65 70 75 80
Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg
85 90 95
Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln
100 105 110
Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala
115 120 125
Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu
130 135 140
Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Cys Arg Glu Lys Gln Tyr Leu Ile Asn Ser Gln Cys Cys Ser Leu
1 5 10 15
Cys Gln Pro Gly Gln Lys Leu Val Ser Asp Cys Thr Glu Phe Thr Glu
20 25 30
Thr Glu Cys Leu Pro Cys Gly Glu Ser Glu Phe Leu Asp Thr Trp Asn
35 40 45
Arg Glu Thr His Cys His Gln His Lys Tyr Cys Asp Pro Asn Leu Gly
50 55 60
Leu Arg Val Gln Gln Lys Gly Thr Ser Glu Thr Asp Thr Ile Cys Thr
65 70 75 80
Cys Glu Glu Gly Trp His Cys Thr Ser Glu Ala Cys Glu Ser Cys Val
85 90 95
Leu His Arg Ser Cys Ser Pro Gly Phe Gly Val Lys Gln Ile Ala Thr
100 105 110
Gly Val Ser Asp Thr Ile Cys Glu Pro Cys Pro Val Gly Phe Phe Ser
115 120 125
Asn Val Ser Ser Ala Phe Glu Lys Cys His Pro Thr Ser Cys Glu Thr
130 135 140
Lys Asp Leu Val Val Gln Gln Ala Gly Thr Asn Lys Thr Asp Val Val
145 150 155 160
Cys Gly

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn Cys Val Lys Asp Thr Tyr Pro Ser Gly His Lys Cys Cys Arg Glu
1 5 10 15
Cys Gln Pro Gly His Gly Met Val Ser Arg Cys Asp His Thr Arg Asp
20 25 30
Thr Val Cys His Asn Cys Val Lys Asp Thr Tyr Pro Ser Gly His Lys
35 40 45
Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val Ser Arg Cys Asp
50 55 60

His Thr Arg Asp Thr Val Cys His Cys Arg Pro Gly Thr Gln Pro Arg
 65 70 75 80
 Gln Asp Ser Ser His Lys Phe Gly Val Asp Cys Val Pro Cys Pro Pro
 85 90 95
 Gly His Phe Ser Pro Gly Ser Asn Gln Ala Cys Lys Pro Trp Thr Asn
 100 105 110
 Cys Thr Leu Ser Gly Lys Gln Ile Arg His Pro Ala Ser Asn Ser Leu
 115 120 125
 Asp Thr Val Cys Glu
 130

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro Asp
 1 5 10 15
 Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu Thr Leu His
 20 25 30
 Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser
 35 40 45

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro Asp
 1 5 10 15
 Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu Thr Leu His
 20 25 30
 Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys	Ala	Pro	His	Pro	Lys	Gln	Glu	Pro	Gln	Glu	Ile	Asn	Phe	Pro	Asp	
1				5				10						15		
Asp	Leu	Pro	Gly	Ser	Asn	Thr	Ala	Ala	Pro	Val	Gln	Glu	Thr	Leu	His	
			20					25					30			
Gly	Cys	Gln	Pro	Val	Thr	Gln	Glu	Asp	Gly	Lys	Glu	Ser				
		35					40					45				